SEQUENCE LISTING

<110> Zavada, Jan
Pastorekova, Silvia
Pastorek, Jaromir

<120> MN Gene and Protein

<130> D-0021.5 PCT

<140>
<141>

<150> 09/177,776
<151> 1998-10-23

<150> 09/178,115
<151> 1998-10-23

<160> 143

<170> PatentIn Ver. 2.0

<210> 1
<211> 1522
<212> DNA
<213> HUMAN

<220>
<221> CDS
<222> (13)..(1389)

<220>
<221> mat_peptide
<222> (124)..(1389)

<400> 1

```
acagtcagcc gc atg gct ccc ctg tgc ccc agc ccc tgg ctc cct ctg ttg 51
              Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu
                      -35                 -30                 -25

atc ccg gcc cct gct cca ggc ctc act gtg caa ctg ctg ctg tca ctg   99
Ile Pro Ala Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu
                -20                 -15                 -10

ctg ctt ctg atg cct gtc cat ccc cag agg ttg ccc cgg atg cag gag   147
Leu Leu Leu Met Pro Val His Pro Gln Arg Leu Pro Arg Met  ln Glu
             -5                -1   1                5
```

```
gat tcc ccc ttg gga gga ggc tct tct ggg gaa gat gac cca ctg ggc   195
Asp Ser Pro Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly
     10                  15                  20

gag gag gat ctg ccc agt gaa gag gat tca ccc aga gag gag gat cca   243
Glu Glu Asp Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro
 25                  30                  35                  40

ccc gga gag gag gat cta cct gga gag gag gat cta cct gga gag gag   291
Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu
                 45                  50                  55

gat cta cct gaa gtt aag cct aaa tca gaa gaa gag ggc tcc ctg aag   339
Asp Leu Pro Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys
             60                  65                  70

tta gag gat cta cct act gtt gag gct cct gga gat cct caa gaa ccc   387
Leu Glu Asp Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro
         75                  80                  85

cag aat aat gcc cac agg gac aaa gaa ggg gat gac cag agt cat tgg   435
Gln Asn Asn Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp
     90                  95                 100

cgc tat gga ggc gac ccg ccc tgg ccc cgg gtg tcc cca gcc tgc gcg   483
Arg Tyr Gly Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala
105                 110                 115                 120

ggc cgc ttc cag tcc ccg gtg gat atc cgc ccc cag ctc gcc gcc ttc   531
Gly Arg Phe Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe
                125                 130                 135

tgc ccg gcc ctg cgc ccc ctg gaa ctc ctg ggc ttc cag ctc ccg ccg   579
Cys Pro Ala Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro
            140                 145                 150

ctc cca gaa ctg cgc ctg cgc aac aat ggc cac agt gtg caa ctg acc   627
Leu Pro Glu Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr
        155                 160                 165

ctg cct cct ggg cta gag atg gct ctg ggt ccc ggg cgg gag tac cgg   675
Leu Pro Pro Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg
    170                 175                 180

gct ctg cag ctg cat ctg cac tgg ggg gct gca ggt cgt ccg ggc tcg   723
Ala Leu Gln Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser
185                 190                 195                 200
```

```
gag cac act gtg gaa ggc cac cgt ttc cct gcc gag atc cac gtg gtt   771
 lu His Thr Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val
                205                 210                 215

cac ctc agc acc gcc ttt gcc aga gtt gac gag gcc ttg ggg cgc ccg   819
His Leu Ser Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro
            220                 225                 230

gga ggc ctg gcc gtg ttg gcc gcc ttt ctg gag gag ggc ccg gaa gaa   867
Gly Gly Leu Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu
        235                 240                 245

aac agt gcc tat gag cag ttg ctg tct cgc ttg gaa gaa atc gct gag   915
Asn Ser Ala Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu
    250                 255                 260

gaa ggc tca gag act cag gtc cca gga ctg gac ata tct gca ctc ctg   963
Glu Gly Ser Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu
265                 270                 275                 280

ccc tct gac ttc agc cgc tac ttc caa tat gag ggg tct ctg act aca   1011
Pro Ser Asp Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr
                285                 290                 295

ccg ccc tgt gcc cag ggt gtc atc tgg act gtg ttt aac cag aca gtg   1059
Pro Pro Cys Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val
            300                 305                 310

atg ctg agt gct aag cag ctc cac acc ctc tct gac acc ctg tgg gga   1107
Met Leu Ser Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly
        315                 320                 325

cct ggt gac tct cgg cta cag ctg aac ttc cga gcg acg cag cct ttg   1155
Pro Gly Asp Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu
    330                 335                 340

aat ggg cga gtg att gag gcc tcc ttc cct gct gga gtg gac agc agt   1203
Asn Gly Arg Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser
345                 350                 355                 360

cct cgg gct gct gag cca gtc cag ctg aat tcc tgc ctg gct gct ggt   1251
Pro Arg Ala Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly
                365                 370                 375

gac atc cta gcc ctg gtt ttt ggc ctc ctt ttt gct gtc acc agc gtc   1299
Asp Ile Leu Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val
            380                 385                 390
```

```
gcg ttc ctt gtg cag atg aga agg cag cac aga agg gga acc aaa ggg   1347
Ala Phe Leu Val  ln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly
        395                 400                 405

ggt gtg agc tac cgc cca gca gag gta gcc gag act gga gcc           1389
Gly Val Ser Tyr Arg Pro Ala Glu Val Ala Glu Thr Gly Ala
    410                 415                 420

tagaggctgg atcttggaga atgtgagaag ccagccagag gcatctgagg gggagccggt 1449

aactgtcctg tcctgctcat tatgccactt ccttttaact gccaagaaat tttttaaaat 1509

aaatatttat aat                                                    1522
```

<210> 2
<211> 459
<212> PRT
<213> HUMAN

<400> 2

```
Met Ala Pro Leu Cys Pro Ser Pro Trp Leu Pro Leu Leu Ile Pro Ala
        -35                 -30                 -25

Pro Ala Pro Gly Leu Thr Val Gln Leu Leu Leu Ser Leu Leu Leu Leu
    -20                 -15                 -10

Met Pro Val His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro
 -5              -1   1                5                  10

Leu Gly Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp
             15                  20                  25

Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu
         30                  35                  40

Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
     45                  50                  55

Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp
 60                  65                  70                  75

Leu Pro Thr Val Glu Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn
                 80                  85                  90

Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly
             95                  100                 105
```

```
Gly Asp Pro Pro Trp Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe
        110                 115                 120

Gln Ser Pro Val Asp Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala
    125                 130                 135

Leu Arg Pro Leu Glu Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu
140                 145                 150                 155

Leu Arg Leu Arg Asn Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro
                160                 165                 170

Gly Leu Glu Met Ala Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln
            175                 180                 185

Leu His Leu His Trp Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr
        190                 195                 200

Val Glu Gly His Arg Phe Pro Ala Glu Ile His Val Val His Leu Ser
    205                 210                 215

Thr Ala Phe Ala Arg Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu
220                 225                 230                 235

Ala Val Leu Ala Ala Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala
                240                 245                 250

Tyr Glu Gln Leu Leu Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser
            255                 260                 265

Glu Thr Gln Val Pro Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp
        270                 275                 280

Phe Ser Arg Tyr Phe Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys
    285                 290                 295

Ala Gln Gly Val Ile Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser
300                 305                 310                 315

Ala Lys Gln Leu His Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp
                320                 325                 330

Ser Arg Leu Gln Leu Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg
            335                 340                 345

Val Ile Glu Ala Ser Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala
        350                 355                 360
```

Ala Glu Pro Val Gln Leu Asn Ser Cys Leu Ala Ala Gly Asp Ile Leu
365 370 375

Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala Phe Leu
380 385 390 395

Val Gln Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser
400 405 410

Tyr Arg Pro Ala Glu Val Ala Glu Thr Gly Ala
415 420

<210> 3
<211> 29
<212> DNA
<213> HUMAN

<400> 3
cgcccagtgg gtcatcttcc ccagaagag 29

<210> 4
<211> 19
<212> DNA
<213> HUMAN

<400> 4
ggaatcctcc tgcatccgg 19

<210> 5
<211> 10898
<212> DNA
<213> HUMAN

<220>
<221> gene
<222> (1)..(10898)

<400> 5
ggatcctgtt gactcgtgac cttaccccca accctgtgct ctctgaaaca tgagctgtgt 60

ccactcaggg ttaaatggat taagggcggt gcaagatgtg ctttgttaaa cagatgcttg 120

aaggcagcat gctcgttaag agtcatcacc aatccctaat ctcaagtaat cagggacaca 180

aacactgcgg aaggccgcag ggtcctctgc ctaggaaaac cagagacctt tgttcacttg 240

tttatctgac cttccctcca ctattgtcca tgaccctgcc aaatcccccc ctgtgagaaa 300

cacccaagaa ttatcaataa aaaaataaat ttaaaaaaaa aatacaaaaa aaaaaaaaaa 360

aaaaaaaaaa gacttacgaa tagttattga taaatgaata gctattggta aagccaagta 420

aatgatcata ttcaaaacca gacggccatc atcacagctc aagtctacct gatttgatct 480

ctttatcatt gtcattcttt ggattcacta gattagtcat catcctcaaa attctccccc 540

aagttctaat tacgttccaa acatttaggg gttacatgaa gcttgaacct actaccttct 600

ttgcttttga gccatgagtt gtaggaatga tgagtttaca ccttacatgc tggggattaa 660

tttaaacttt acctctaagt cagttgggta gcctttggct tatttttgta gctaattttg 720

tagttaatgg atgcactgtg aatcttgcta tgatagtttt cctccacact ttgccactag 780

gggtaggtag gtactcagtt ttcagtaatt gcttacctaa gaccctaagc cctatttctc 840

ttgtactggc ctttatctgt aatatgggca tatttaatac aatataattt ttggagtttt 900

tttgtttgtt tgtttgtttg ttttttttgag acggagtctt gcatctgtca tgcccaggct 960

ggagtagcag tggtgccatc tcggctcact gcaagctcca cctcccgagt tcacgccatt 1020

ttcctgcctc agcctcccga gtagctggga ctacaggcgc ccgccaccat gcccggctaa 1080

ttttttgtat ttttggtaga gacggggttt caccgtgtta gccagaatgg tctcgatctc 1140

ctgacttcgt gatccacccg cctcggcctc ccaaagttct gggattacag gtgtgagcca 1200

ccgcacctgg ccaatttttt gagtctttta aagtaaaaat atgtcttgta agctggtaac 1260

tatggtacat ttccttttat taatgtggtg ctgacggtca tataggttct tttgagtttg 1320

gcatgcatat gctacttttt gcagtccttt cattacattt ttctctcttc atttgaagag 1380

catgttatat cttttagctt cacttggctt aaaaggttct ctcattagcc taacacagtg 1440

tcattgttgg taccacttgg atcataagtg gaaaaacagt caagaaattg cacagtaata 1500

cttgtttgta agagggatga ttcaggtgaa tctgacacta agaaactccc ctacctgagg 1560

tctgagattc ctctgacatt gctgtatata ggcttttcct ttgacagcct gtgactgcgg 1620

actatttttc ttaagcaaga tatgctaaag ttttgtgagc ctttttccag agagaggtct 1680

catatctgca tcaagtgaga acatataatg tctgcatgtt tccatatttc aggaatgttt 1740

gcttgtgttt tatgctttta tatagacagg gaaacttgtt cctcagtgac ccaaaagagg 1800

tgggaattgt tattggatat catcattggc ccacgctttc tgaccttgga aacaattaag 1860

ggttcataat ctcaattctg tcagaattgg tacaagaaat agctgctatg tttcttgaca 1920

ttccacttgg taggaaataa gaatgtgaaa ctcttcagtt ggtgtgtgtc cctngttttt 1980

ttgcaatttc cttcttactg tgttaaaaaa aagtatgatc ttgctctgag aggtgaggca 2040

ttcttaatca tgatctttaa agatcaataa tataatcctt tcaaggatta tgtctttatt 2100

ataataaaga taatttgtct ttaacagaat caataatata atcccttaaa ggattatatc 2160

tttgctgggc gcagtggctc acacctgtaa tcccagcact ttgggtggcc aaggtggaag 2220

gatcaaattt gcctacttct atattatctt ctaaagcaga attcatctct cttccctcaa 2280

tatgatgata ttgacagggt ttgccctcac tcactagatt gtgagctcct gctcagggca 2340

ggtagcgttt tttgtttttg tttttgtttt tctttttttga gacagggtct tgctctgtca 2400

cccaggccag agtgcaatgg tacagtctca gctcactgca gcctcaaccg cctcggctca 2460

aaccatcatc ccatttcagc ctcctgagta gctgggacta caggcacatg ccattacacc 2520

tggctaattt ttttgtattt ctagtagaga cagggtttgg ccatgttgcc cgggctggtc 2580

tcgaactcct ggactcaagc aatccaccca cctcagcctc ccaaaatgag ggaccgtgtc 2640

ttattcattt ccatgtccct agtccatagc ccagtgctgg acctatggta gtactaaata 2700

aatatttgtt gaatgcaata gtaaatagca tttcagggag caagaactag attaacaaag 2760

gtggtaaaag gtttggagaa aaaaataata gtttaatttg gctagagtat gagggagagt 2820

agtaggagac aagatggaaa ggtctcttgg gcaaggtttt gaaggaagtt ggaagtcaga 2880

agtacacaat gtgcatatcg tggcaggcag tggggagcca atgaaggctt ttgagcagga 2940

gagtaatgtg ttgaaaaata aatataggtt aaacctatca gagcccctct gacacataca 3000

cttgcttttc attcaagctc aagtttgtct cccacatacc cattacttaa ctcaccctcg 3060

ggctccccta gcagcctgcc ctacctcttt acctgcttcc tggtggagtc agggatgtat 3120

acatgagctg ctttccctct cagccagagg acatgggggg ccccagctcc cctgcctttc 3180

cccttctgtg cctggagctg ggaagcaggc cagggttagc tgaggctggc tggcaagcag 3240

ctgggtggtg ccagggagag cctgcatagt gccaggtggt gccttgggtt ccaagctagt 3300

ccatggcccc gataaccttc tgcctgtgca cacacctgcc cctcactcca cccccatcct 3360

agctttggta tgggggagag ggcacagggc cagacaaacc tgtgagactt tggctccatc 3420

tctgcaaaag ggcgctctgt gagtcagcct gctcccctcc aggcttgctc ctccccccacc 3480

cagctctcgt ttccaatgca cgtacagccc gtacacaccg tgtgctggga caccccacag 3540

tcagccgcat ggctcccctg tgccccagcc cctggctccc tctgttgatc ccggcccctg 3600

ctccaggcct cactgtgcaa ctgctgctgt cactgctgct tctggtgcct gtccatcccc 3660

agaggttgcc ccggatgcag gaggattccc ccttgggagg aggctcttct ggggaagatg 3720

acccactggg cgaggaggat ctgcccagtg aagaggattc acccagagag gaggatccac 3780

ccggagagga ggatctacct ggagaggagg atctacctgg agaggaggat ctacctgaag 3840

ttaagcctaa atcagaagaa gagggctccc tgaagttaga ggatctacct actgttgagg 3900

ctcctggaga tcctcaagaa ccccagaata atgcccacag ggacaaagaa ggtaagtggt 3960

catcaatctc caaatccagg ttccaggagg ttcatgactc ccctcccata ccccagccta 4020

ggctctgttc actcagggaa ggaggggaga ctgtactccc cacagaagcc cttccagagg 4080

tcccatacca atatccccat ccccactctc ggaggtagaa agggacagat gtggagagaa 4140

aataaaaagg gtgcaaaagg agagaggtga gctggatgag atgggagaga agggggaggc 4200

tggagaagag aaagggatga gaactgcaga tgagagaaaa aatgtgcaga cagaggaaaa 4260

aaataggtgg agaaggagag tcagagagtt tgaggggaag agaaaaggaa agcttgggag 4320

gtgaagtggg taccagagac aagcaagaag agctggtaga agtcatctca tcttaggcta 4380

caatgaggaa ttgagaccta ggaagaaggg acacagcagg tagagaaacg tggcttcttg 4440

actcccaagc caggaatttg gggaaagggg ttggagacca tacaaggcag agggatgagt 4500

ggggagaaga aagaagggag aaaggaaaga tggtgtactc actcatttgg gactcaggac 4560

tgaagtgccc actcactttt ttttttttt tttttgagac aaactttcac ttttgttgcc 4620

caggctggag tgcaatggcg cgatctcggc tcactgcaac ctccacctcc cgggttcaag 4680

tgattctcct gcctcagcct ctagccaagt agctgcgatt acaggcatgc gccaccacgc 4740

ccggctaatt tttgtatttt tagtagagac ggggtttcgc catgttggtc aggctggtct 4800

cgaactcctg atctcaggtg atccaaccac cctggcctcc caaagtgctg ggattatagg 4860

cgtgagccac agcgcctggc ctgaagcagc cactcacttt tacagaccct aagacaatga 4920

ttgcaagctg gtaggattgc tgtttggccc acccagctgc ggtgttgagt ttgggtgcgg 4980

tctcctgtgc tttgcacctg gcccgcttaa ggcatttgtt acccgtaatg ctcctgtaag 5040

gcatctgcgt ttgtgacatc gttttggtcg ccaggaaggg attggggctc taagcttgag 5100

cggttcatcc ttttcattta tacaggggat gaccagagtc attggcgcta tggaggtgag 5160

acacccaccc gctgcacaga cccaatctgg gaacccagct ctgtggatct cccctacagc 5220

cgtccctgaa cactggtccc gggcgtccca cccgccgccc accgtcccac cccctcacct 5280

tttctacccg ggttccctaa gttcctgacc taggcgtcag acttcctcac tatactctcc 5340

caccccaggc gacccgccct ggccccgggt gtccccagcc tgcgcgggcc gcttccagtc 5400

cccggtggat atccgccccc agctcgccgc cttctgcccg gccctgcgcc ccctggaact 5460

cctgggcttc cagctcccgc cgctcccaga actgcgcctg cgcaacaatg gccacagtgg 5520

tgaggggGtc tccccgccga gacttgggga tggggcgggg cgcagggaag ggaaccgtcg 5580

cgcagtgcct gcccgggggt tgggctggcc ctaccgggcg gggccggctc acttgcctct 5640

ccctacgcag tgcaactgac cctgcctcct gggctagaga tggctctggg tcccgggcgg 5700

gagtaccggg ctctgcagct gcatctgcac tgggggggctg caggtcgtcc gggctcggag 5760

cacactgtgg aaggccaccg tttccctgcc gaggtgagcg cggactggcc gagaaggggc 5820

aaaggagcgg ggcggacggg ggccagagac gtggccctct cctaccctcg tgtcctttтc 5880

agatccacgt ggttcacctc agcaccgcct ttgccagagt tgacgaggcc ttggggcgcc 5940

cgggaggcct ggccgtgttg gccgcctttc tggaggtacc agatcctgga caccccctac 6000

tccccgcttt cccatcccat gctcctcccg gactctatcg tggagccaga gaccccatcc 6060

cagcaagctc actcaggccc ctggctgaca aactcattca cgcactgttt gttcatttaa 6120

cacccactgt gaaccaggca ccagccccca acaaggattc tgaagctgta ggtccttgcc 6180

tctaaggagc ccacagccag tgggggaggc tgacatgaca gacacatagg aaggacatag 6240

taaagatggt ggtcacagag gaggtgacac ttaaagcctt cactggtaga aaagaaaagg 6300

aggtgttcat tgcagaggaa acagaatgtg caaagactca gaatatggcc tatttaggga 6360

atggctacat acaccatgat tagaggaggc ccagtaaagg gaagggatgg tgagatgcct 6420

gctaggttca ctcactcact tttatttatt tatttatttt tttgacagtc tctctgtcgc 6480

ccaggctgga gtgcagtggt gtgatcttgg gtcactgcaa cttccgcctc ccgggttcaa 6540

gggattctcc tgcctcagct tcctgagtag ctggggttac aggtgtgtgc caccatgccc 6600

agctaatttt tttttgtatt tttagtagac agggtttcac catgttggtc aggctggtct 6660

caaactcctg gcctcaagtg atccgcctga ctcagcctac caaagtgctg attacaagtg 6720

tgagccaccg tgcccagcca cactcactga ttctttaatg ccagccacac agcacaaagt 6780

tcagagaaat gcctccatca tagcatgtca atatgttcat actcttaggt tcatgatgtt 6840

cttaacatta ggttcataag caaaataaga aaaaagaata ataaataaaa gaagtggcat 6900

gtcaggacct cacctgaaaa gccaaacaca gaatcatgaa ggtgaatgca gaggtgacac 6960

caacacaaag gtgtatatat ggtttcctgt ggggagtatg tacggaggca gcagtgagtg 7020

agactgcaaa cgtcagaagg gcacgggtca ctgagagcct agtatcctag taaagtgggc 7080

tctctccctc tctctccagc ttgtcattga aaaccagtcc accaagcttg ttggttcgca 7140

cagcaagagt acatagagtt tgaaataata cataggattt taagagggag acactgtctc 7200

taaaaaaaaa aacaacagca acaacaaaaa gcaacaacca ttacaatttt atgttccctc 7260

agcattctca gagctgagga atgggagagg actatgggaa ccccccttcat gttccggcct 7320

tcagccatgg ccctggatac atgcactcat ctgtcttaca atgtcattcc cccaggaggg 7380

cccggaagaa aacagtgcct atgagcagtt gctgtctcgc ttggaagaaa tcgctgagga 7440

aggtcagttt gttggtctgg ccactaatct ctgtggccta gttcataaag aatcaccctt 7500

tggagcttca ggtctgaggc tggagatggg ctccctccag tgcaggaggg attgaagcat 7560

gagccagcgc tcatcttgat aataaccatg aagctgacag acacagttac ccgcaaacgg 7620

ctgcctacag attgaaaacc aagcaaaaac cgccgggcac ggtggctcac gcctgtaatc 7680

ccagcacttt gggaggccaa ggcaggtgga tcacgaggtc aagagatcaa gaccatcctg 7740

gccaacatgg tgaaacccca tctctactaa aaatacgaaa aaatagccag gcgtggtggc 7800

gggtgcctgt aatcccagct actcgggagg ctgaggcagg agaatggcat gaacccggga 7860

ggcagaagtt gcagtgagcc gagatcgtgc cactgcactc cagcctgggc aacagagcga 7920

gactcttgtc tcaaaaaaaa aaaaaaaaaa gaaaaccaag caaaaaccaa aatgagacaa 7980

aaaaaacaag accaaaaaat ggtgtttgga aattgtcaag gtcaagtctg gagagctaaa 8040

ctttttctga gaactgttta tctttaataa gcatcaaata ttttaacttt gtaaatactt 8100

ttgttggaaa tcgttctctt cttagtcact cttgggtcat tttaaatctc acttactcta 8160

ctagaccttt taggtttctg ctagactagg tagaactctg cctttgcatt tcttgtgtct 8220

gttttgtata gttatcaata ttcatattta tttacaagtt attcagatca ttttttcttt 8280

tctttttttt ttttttttt ttttttacat ctttagtaga gacagggttt caccatattg 8340

gccaggctgc tctcaaactc ctgaccttgt gatccaccag cctcggcctc ccaaagtgct 8400

gggattcatt ttttcttttt aatttgctct gggcttaaac ttgtggccca gcactttatg 8460

atggtacaca gagttaagag tgtagactca gacggtcttt cttctttcct tctcttcctt 8520

cctcccttcc ctcccacctt cccttctctc cttcctttct ttcttcctct cttgcttcct 8580

caggcctctt ccagttgctc caaagccctg tacttttttt tgagttaacg tcttatggga 8640

agggcctgca cttagtgaag aagtggtctc agagttgagt taccttggct tctgggaggt 8700

gaaactgtat ccctataccc tgaagcttta agggggtgca atgtagatga gaccccaaca 8760

tagatcctct tcacaggctc agagactcag gtcccaggac tggacatatc tgcactcctg 8820

ccctctgact tcagccgcta cttccaatat gaggggtctc tgactacacc gccctgtgcc 8880

cagggtgtca tctggactgt gtttaaccag acagtgatgc tgagtgctaa gcaggtgggc 8940

ctggggtgtg tgtggacaca gtgggtgcgg gggaaagagg atgtaagatg agatgagaaa 9000

caggagaaga aagaaatcaa ggctgggctc tgtggcttac gcctataatc ccaccacgtt 9060

gggaggctga ggtgggagaa tggtttgagc ccaggagttc aagacaaggc ggggcaacat 9120

agtgtgaccc catctctacc aaaaaaaccc caacaaaacc aaaaatagcc gggcatggtg 9180

gtatgcggcc tagtcccagc tactcaagga ggctgaggtg ggaagatcgc ttgattccag 9240

gagtttgaga ctgcagtgag ctatgatccc accactgcct accatcttta ggatacattt 9300

atttatttat aaaagaaatc aagaggctgg atggggaata caggagctgg agggtggagc 9360

cctgaggtgc tggttgtgag ctggcctggg acccttgttt cctgtcatgc catgaaccca 9420

cccacactgt ccactgacct ccctagctcc acaccctctc tgacaccctg tggggacctg 9480

gtgactctcg gctacagctg aacttccgag cgacgcagcc tttgaatggg cgagtgattg 9540

aggcctcctt ccctgctgga gtggacagca gtcctcgggc tgctgagcca ggtacagctt 9600

tgtctggttt ccccccagcc agtagtccct tatcctccca tgtgtgtgcc agtgtctgtc 9660

attggtggtc acagcccgcc tctcacatct ccttttttctc tccagtccag ctgaattcct 9720

gcctggctgc tggtgagtct gcccctcctc ttggtcctga tgccaggaga ctcctcagca 9780

ccattcagcc ccagggctgc tcaggaccgc ctctgctccc tctccttttc tgcagaacag 9840

accccaaccc caatattaga gaggcagatc atggtgggga ttcccccatt gtccccagag 9900

gctaattgat tagaatgaag cttgagaaat ctcccagcat ccctctcgca aaagaatccc 9960

ccccccttttt tttaaagata gggtctcact ctgtttgccc caggctgggg tgttgtggca 10020

cgatcatagc tcactgcagc ctcgaactcc taggctcagg caatcctttc accttagctt 10080

ctcaaagcac tgggactgta ggcatgagcc actgtgcctg gccccaaacg gccctttttac 10140

ttggctttta ggaagcaaaa acggtgctta tcttaccccct tctcgtgtat ccaccctcat 10200

cccttggctg gcctcttctg gagactgagg cactatgggg ctgcctgaga actcggggca 10260

ggggtggtgg agtgcactga ggcaggtgtt gaggaactct gcagacccct cttccttccc 10320

aaagcagccc tctctgctct ccatcgcagg tgacatccta gccctggttt ttggcctcct 10380

ttttgctgtc accagcgtcg cgttccttgt gcagatgaga aggcagcaca ggtattacac 10440

tgacccttte ttcaggcaca agcttccccc acccttgtgg agtcacttca tgcaaagcgc 10500

atgcaaatga gctgctcctg ggccagtttt ctgattagcc tttcctgttg tgtacacaca 10560

gaaggggaac caaagggggt gtgagctacc gcccagcaga ggtagccgag actggagcct 10620

agaggctgga tcttggagaa tgtgagaagc cagccagagg catctgaggg ggagccggta 10680

actgtcctgt cctgctcatt atgccacttc cttttaactg ccaagaaatt ttttaaaata 10740

aatatttata ataaaatatg tgttagtcac ctttgttccc caaatcagaa ggaggtattt 10800

gaatttccta ttactgttat tagcaccaat ttagtggtaa tgcatttatt ctattacagt 10860

tcggcctcct tccacacatc actccaatgt gttgctcc 10898

<210> 6
<211> 37
<212> PRT
<213> HUMAN

<400> 6

Met	Ala	Pro	Leu	Cys	Pro	Ser	Pro	Trp	Leu	Pro	Leu	Leu	Ile	Pro	Ala				
1				5					10						15				
Pro	Ala	Pro	Gly	Leu	Thr	Val	Gln	Leu	Leu	Leu	Ser	Leu	Leu	Leu	Leu				
			20					25					30						
Met	Pro	Val	His	Pro															
			35																

<210> 7
<211> 25
<212> DNA
<213> HUMAN

<400> 7
tggggttctt gaggatctcc aggag 25

<210> 8
<211> 26
<212> DNA
<213> HUMAN

<400> 8
ctctaacttc agggagccct cttctt 26

<210> 9
<211> 48
<212> DNA
<213> HUMAN

<220>
<221> primer_bind
<222> (1)..(48)

<400> 9
cuacuacuac uaggccacgc gtcgactagt acgggnnggg nngggnng 48

<210> 10
<211> 6
<212> PRT
<213> HUMAN

<400> 10
Glu Glu Asp Leu Pro Ser
1 5

<210> 11
<211> 6
<212> PRT
<213> HUMAN

<400> 11
Gly Glu Asp Asp Pro Leu
1 5

<210> 12
<211> 21
<212> PRT
<213> HUMAN

<400> 12

Asn Asn Ala His Arg Asp Lys Glu Gly Asp Asp Gln Ser His Trp Arg
1 5 10 15

Tyr Gly Gly Asp Pro
20

<210> 13
<211> 16
<212> PRT
<213> HUMAN

<400> 13
His Pro Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro Leu Gly Gly
1 5 10 15

<210> 14
<211> 24
<212> PRT
<213> HUMAN

<400> 14
Glu Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu
1 5 10 15

Pro Gly Glu Glu Asp Leu Pro Gly
20

<210> 15
<211> 13
<212> PRT
<213> HUMAN

<400> 15
Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln
1 5 10

<210> 16
<211> 16
<212> PRT
<213> HUMAN

<400> 16
Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg
1 5 10 15

<210> 17
<211> 45
<212> DNA
<213> HUMAN

<400> 17
gtcgctagct ccatgggtca tatgcagagg ttgccccgga tgcag 45

<210> 18
<211> 43
<212> DNA
<213> HUMAN

<400> 18
gaagatctct tactcgagca ttctccaaga tccagcctct agg 43

<210> 19
<211> 10
<212> DNA
<213> HUMAN

<400> 19
ctccatctct 10

<210> 20
<211> 10
<212> DNA
<213> HUMAN

<400> 20
ccacccccat 10

<210> 21
<211> 205
<212> DNA
<213> HUMAN

<400> 21
acctgccccc cactccaccc ccatcctagc tttggtatgg gggagagggc acagggccag 60

acaaacctgt gagactttgg ctccatctct gcaaaagggc gctctgtgag tcagcctgct 120

ccctccagg cttgctcctc ccccacccag ctctcgtttc caatgcacgt acagcccgta 180

cacaccgtgt gctgggacac cccac 205

<210> 22
<211> 8
<212> PRT
<213> HUMAN

<400> 22
Leu Glu His His His His His His
1 5

<210> 23
<211> 10
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(10)

<400> 23
yyycayyyyy 10

<210> 24
<211> 10
<212> DNA
<213> HUMAN

<300>
<301> Locker and Buzard,
<303> DNA Sequencing and Mapping
<304> 1
<306> 3-11
<307> 1990

<400> 24
tgtgagactt 10

<210> 25
<211> 4
<212> PRT
<213> HUMAN

<220>
<221> SITE
<222> (1)..(4)

<400> 25
Ser Pro Xaa Xaa
1

<210> 26
<211> 4
<212> PRT
<213> HUMAN

<220>
<221> SITE
<222> (1)..(4)

<400> 26
Thr Pro Xaa Xaa
1

<210> 27
<211> 540
<212> DNA
<213> HUMAN

<220>
<221> promoter
<222> (1)..(540)

<400> 27
cttgcttttc attcaagctc aagtttgtct cccacatacc cattacttaa ctcaccctcg 60

ggctccccta gcagcctgcc ctacctcttt acctgcttcc tggtggagtc agggatgtat 120

acatgagctg ctttccctct cagccagagg acatgggggg ccccagctcc cctgcctttc 180

cccttctgtg cctggagctg ggaagcaggc cagggttagc tgaggctggc tggcaagcag 240

ctgggtggtg ccagggagag cctgcatagt gccaggtggt gccttgggtt ccaagctagt 300

ccatggcccc gataaccttc tgcctgtgca cacacctgcc cctcactcca cccccatcct 360

agctttggta tgggggagag ggcacagggc cagacaaacc tgtgagactt tggctccatc 420

tctgcaaaag ggcgctctgt gagtcagcct gctcccctcc aggcttgctc ctcccccacc 480

cagctctcgt ttccaatgca cgtacagccc gtacacaccg tgtgctggga caccccacag 540

<210> 28
<211> 445
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 1st MN exon

<400> 28
gcccgtacac accgtgtgct gggacacccc acagtcagcc gcatggctcc 50

cctgtgcccc agcccctggc tccctctgtt gatcccggcc cctgctccag 100

gcctcactgt gcaactgctg ctgtcactgc tgcttctggt gcctgtccat 150

ccccagaggt tgccccggat gcaggaggat tccccttgg gaggaggctc 200

ttctggggaa gatgacccac tgggcgagga ggatctgccc agtgaagagg 250

attcacccag agaggaggat ccacccggag aggaggatct acctggagag 300

gaggatctac ctggagagga ggatctacct gaagttaagc ctaaatcaga 350

agaagagggc tccctgaagt tagaggatct acctactgtt gaggctcctg 400

gagatcctca agaaccccag aataatgccc acagggacaa agaag 445

<210> 29
<211> 30
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 2nd MN exon

<400> 29
gggatgacca gagtcattgg cgctatggag 30

<210> 30
<211> 171
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 3rd MN exon

<400> 30
gcgacccgcc ctggccccgg gtgtccccag cctgcgcggg ccgcttccag 50

tccccggtgg atatccgccc ccagctcgcc gccttctgcc cggccctgcg 100

ccccctggaa ctcctgggct tccagctccc gccgctccca gaactgcgcc 150

tgcgcaacaa tggccacagt g 171

<210> 31
<211> 143
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 4th MN exon

<400> 31
tgcaactgac cctgcctcct gggctagaga tggctctggg tcccgggcgg 50

gagtaccggg ctctgcagct gcatctgcac tgggggggctg caggtcgtcc 100

gggctcggag cacactgtgg aaggccaccg tttccctgcc gag 143

<210> 32
<211> 93
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 5th MN exon

<400> 32
atccacgtgg ttcacctcag caccgccttt gccagagttg acgaggcctt 50

ggggcgcccg ggaggcctgg ccgtgttggc cgcctttctg gag 93

<210> 33
<211> 67
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 6th MN exon

<400> 33
gagggcccgg aagaaaacag tgcctatgag cagttgctgt ctcgcttgga 50

agaaatcgct gaggaag 67

<210> 34
<211> 158
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 7th MN exon

<400> 34
gctcagagac tcaggtccca ggactggaca tatctgcact cctgccctct 50

gacttcagcc gctacttcca atatgagggg tctctgacta caccgccctg 100

tgcccagggt gtcatctgga ctgtgtttaa ccagacagtg atgctgagtg ctaagcag 158

<210> 35
<211> 145
<212> DNA
<213> HUMAN

<220>
<221> exon

<222> (1)
<223> 8th MN exon

<400> 35
ctccacaccc tctctgacac cctgtgggga cctggtgact ctcggctaca 50

gctgaacttc cgagcgacgc agcctttgaa tgggcgagtg attgaggcct 100

ccttccctgc tggagtggac agcagtcctc gggctgctga gccag 145

<210> 36
<211> 27
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 9th MN exon

<400> 36
tccagctgaa ttcctgcctg gctgctg 27

<210> 37
<211> 82
<212> DNA
<213> HUMAN

<220>
<221> exon
<222> (1)
<223> 10th MN exon

<400> 37
gtgacatcct agccctggtt tttggcctcc tttttgctgt caccagcgtc 50

gcgttccttg tgcagatgag aaggcagcac ag 82

<210> 38
<211> 191
<212> DNA
<213> HUMAN

<220>
<221> exon

<222> (1)
<223> 11th MN exon

<400> 38
aaggggaacc aaaggggtg tgagctaccg cccagcagag gtagccgaga 50

ctggagccta gaggctggat cttggagaat gtgagaagcc agccagaggc 100

atctgagggg gagccggtaa ctgtcctgtc ctgctcatta tgccacttcc 150

ttttaactgc caagaaattt tttaaaataa atatttataa t 191

<210> 39
<211> 1174
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(1174)
<223> 1st MN intron

<400> 39
gtaagtggtc atcaatctcc aaatccaggt tccaggaggt tcatgactcc cctcccatac 60

cccagcctag gctctgttca ctcagggaag gaggggagac tgtactcccc acagaagccc 120

ttccagaggt cccataccaa tatccccatc cccactctcg gaggtagaaa gggacagatg 180

tggagagaaa ataaaaaggg tgcaaaagga gagaggtgag ctggatgaga tgggagagaa 240

gggggaggct ggagaagaga aagggatgag aactgcagat gagagaaaaa atgtgcagac 300

agaggaaaaa aataggtgga gaaggagagt cagagagttt gaggggaaga gaaaaggaaa 360

gcttgggagg tgaagtgggt accagagaca agcaagaaga gctggtagaa gtcatctcat 420

cttaggctac aatgaggaat tgagacctag gaagaaggga cacagcaggt agagaaacgt 480

ggcttcttga ctcccaagcc aggaatttgg ggaaaggggt tggagaccat acaaggcaga 540

gggatgagtg gggagaagaa agaagggaga aaggaaagat ggtgtactca ctcatttggg 600

actcaggact gaagtgccca ctcacttttt ttttttttt ttttgagaca aactttcact 660

tttgttgccc aggctggagt gcaatggcgc gatctcggct cactgcaacc tccacctccc 720

gggttcaagt gattctcctg cctcagcctc tagccaagta gctgcgatta caggcatgcg 780

ccaccacgcc cggctaattt ttgtattttt agtagagacg gggtttcgcc atgttggtca 840

ggctggtctc gaactcctga tctcaggtga tccaaccacc ctggcctccc aaagtgctgg 900

gattataggc gtgagccaca gcgcctggcc tgaagcagcc actcactttt acagacccta 960

agacaatgat tgcaagctgg taggattgct gtttggccca cccagctgcg gtgttgagtt 1020

tgggtgcggt ctcctgtgct ttgcacctgg cccgcttaag gcatttgtta cccgtaatgc 1080

tcctgtaagg catctgcgtt tgtgacatcg ttttggtcgc caggaaggga ttggggctct 1140

aagcttgagc ggttcatcct tttcatttat acag 1174

<210> 40
<211> 193
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(193)
<223> 2nd MN intron

<400> 40
gtgagacacc cacccgctgc acagacccaa tctgggaacc cagctctgtg gatctcccct 60

acagccgtcc ctgaacactg gtcccgggcg tcccacccgc cgcccaccgt cccacccccc 120

caccttttct acccgggttc cctaagttcc tgacctaggc gtcagacttc ctcactatac 180

tctcccaccc cag 193

<210> 41
<211> 131
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(131)
<223> 3rd MN intron

<400> 41

gtgaggggt ctccccgccg agacttgggg atggggcggg gcgcagggaa gggaaccgtc 60

gcgcagtgcc tgcccggggg ttgggctggc cctaccgggc ggggccggct cacttgcctc 120

tccctacgca g 131

<210> 42
<211> 89
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(89)
<223> 4th MN intron

<400> 42
gtgagcgcgg actggccgag aaggggcaaa ggagcggggc ggacgggggc cagagacgtg 60

gccctctcct accctcgtgt ccttttcag 89

<210> 43
<211> 1400
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(1400)
<223> 5th MN intron

<400> 43
gtaccagatc ctggacaccc cctactcccc gctttcccat cccatgctcc tcccggactc 60

tatcgtggag ccagagaccc catcccagca agctcactca ggcccctggc tgacaaactc 120

attcacgcac tgtttgttca tttaacaccc actgtgaccc aggcaccagc ccccaacaag 180

gattctgaag ctgtaggtcc ttgcctctaa ggagcccaca gccagtgggg gaggctgaca 240

tgacagacac ataggaagga catagtaaag atggtggtca cagaggaggt gacacttaaa 300

gccttcactg gtagaaaaga aaaggaggtg ttcattgcag aggaaacaga atgtgcaaag 360

actcagaata tggcctattt agggaatggc tacatacacc atgattagag gaggcccagt 420

aaagggaagg gatggtgaga tgcctgctag gttcactcac tcacttttat ttatttattt 480

attttttga cagtctctct gtcgcccagg ctggagtgca gtggtgtgat cttgggtcac 540

tgcaacttcc gcctcccggg ttcaagggat tctcctgcct cagcttcctg agtagctggg 600

gttacaggtg tgtgccacca tgcccagcta attttttttt gtatttttag tagacagggt 660

ttcaccatgt tggtcaggct ggtctcaaac tcctggcctc aagtgatccg cctgactcag 720

cctaccaaag tgctgattac aagtgtgagc caccgtgccc agccacactc actgattctt 780

taatgccagc cacacagcac aaagttcaga gaaatgcctc catcatagca tgtcaatatg 840

ttcatactct taggttcatg atgttcttaa cattaggttc ataagcaaaa taagaaaaaa 900

gaataataaa taaaagaagt ggcatgtcag gacctcacct gaaaagccaa acacagaatc 960

atgaaggtga atgcagaggt gacaccaaca caaaggtgta tatatggttt cctgtgggga 1020

gtatgtacgg aggcagcagt gagtgagact gcaaacgtca gaagggcacg ggtcactgag 1080

agcctagtat cctagtaaag tgggctctct ccctctctct ccagcttgtc attgaaaacc 1140

agtccaccaa gcttgttggt tcgcacagca agagtacata gagtttgaaa taatacatag 1200

gattttaaga gggagacact gtctctaaaa aaaaaaacaa cagcaacaac aaaaagcaac 1260

aaccattaca attttatgtt ccctcagcat tctcagagct gaggaatggg agaggactat 1320

gggaaccccc ttcatgttcc ggccttcagc catggccctg gatacatgca ctcatctgtc 1380

ttacaatgtc attcccccag 1400

<210> 44
<211> 1334
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(1334)
<223> 6th MN intron

<400> 44
gtcagtttgt tggtctggcc actaatctct gtggcctagt tcataaagaa tcacccttttg 60

gagcttcagg tctgaggctg gagatgggct ccctccagtg caggagggat tgaagcatga 120

gccagcgctc atcttgataa taaccatgaa gctgacagac acagttaccc gcaaacggct 180

gcctacagat tgaaaaccaa gcaaaaaccg ccgggcacgg tggctcacgc ctgtaatccc 240

agcactttgg gaggccaagg caggtggatc acgaggtcaa gagatcaaga ccatcctggc 300

caacatggtg aaaccccatc tctactaaaa atacgaaaaa atagccaggc gtggtggcgg 360

gtgcctgtaa tcccagctac tcgggaggct gaggcaggag aatggcatga acccgggagg 420

cagaagttgc agtgagccga gatcgtgcca ctgcactcca gcctgggcaa cagagcgaga 480

ctcttgtctc aaaaaaaaaa aaaaaaaaga aaaccaagca aaaaccaaaa tgagacaaaa 540

aaaacaagac caaaaaatgg tgtttggaaa ttgtcaaggt caagtctgga gagctaaact 600

ttttctgaga actgtttatc tttaataagc atcaaatatt ttaactttgt aaatactttt 660

gttggaaatc gttctcttct tagtcactct tgggtcattt taaatctcac ttactctact 720

agacctttta ggtttctgct agactaggta gaactctgcc tttgcatttc ttgtgtctgt 780

tttgtatagt tatcaatatt catatttatt tacaagttat tcagatcatt ttttcttttc 840

ttttttttt ttttttttt ttttacatct ttagtagaga cagggtttca ccatattggc 900

caggctgctc tcaaactcct gaccttgtga tccaccagcc tcggcctccc aaagtgctgg 960

gattcatttt ttctttttaa tttgctctgg gcttaaactt gtggcccagc actttatgat 1020

ggtacacaga gttaagagtg tagactcaga cggtctttct tctttccttc tcttccttcc 1080

tcccttccct cccaccttcc cttctctcct tcctttcttt cttcctctct tgcttcctca 1140

ggcctcttcc agttgctcca aagccctgta ctttttttg agttaacgtc ttatgggaag 1200

ggcctgcact tagtgaagaa gtggtctcag agttgagtta ccttggcttc tgggaggtga 1260

aactgtatcc ctataccctg aagctttaag ggggtgcaat gtagatgaga ccccaacata 1320

gatcctcttc acag 1334

<210> 45
<211> 512
<212> DNA

<213> HUMAN

<220>
<221> intron
<222> (1)..(512)
<223> 7th MN intron

<400> 45
gtgggcctgg ggtgtgtgtg gacacagtgg gtgcggggga aagaggatgt aagatgagat 60

gagaaacagg agaagaaaga aatcaaggct gggctctgtg gcttacgcct ataatcccac 120

cacgttggga ggctgaggtg ggagaatggt ttgagcccag gagttcaaga caaggcgggg 180

caacatagtg tgaccccatc tctaccaaaa aaaccccaac aaaaccaaaa atagccgggc 240

atggtggtat gcggcctagt cccagctact caaggaggct gaggtgggaa gatcgcttga 300

ttccaggagt ttgagactgc agtgagctat gatcccacca ctgcctacca tctttaggat 360

acatttattt atttataaaa gaaatcaaga ggctggatgg ggaatacagg agctggaggg 420

tggagccctg aggtgctggt tgtgagctgg cctgggaccc ttgtttcctg tcatgccatg 480

aacccaccca cactgtccac tgacctccct ag 512

<210> 46
<211> 114
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(114)
<223> 8th MN intron

<400> 46
gtacagcttt gtctggtttc cccccagcca gtagtccctt atcctcccat gtgtgtgcca 60

gtgtctgtca ttggtggtca cagcccgcct ctcacatctc ctttttctct ccag 114

<210> 47
<211> 617
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(617)
<223> 9th MN intron

<400> 47
gtgagtctgc ccctcctctt ggtcctgatg ccaggagact cctcagcacc attcagcccc 60

agggctgctc aggaccgcct ctgctccctc tccttttctg cagaacagac cccaacccca 120

atattagaga ggcagatcat ggtggggatt cccccattgt ccccagaggc taattgatta 180

gaatgaagct tgagaaatct cccagcatcc ctctcgcaaa agaatccccc ccccttttt 240

taaagatagg gtctcactct gtttgcccca ggctggggtg ttgtggcacg atcatagctc 300

actgcagcct cgaactccta ggctcaggca atcctttcac cttagcttct caaagcactg 360

ggactgtagg catgagccac tgtgcctggc cccaaacggc ccttttactt ggcttttagg 420

aagcaaaaac ggtgcttatc ttacccccttc tcgtgtatcc accctcatcc cttggctggc 480

ctcttctgga gactgaggca ctatggggct gcctgagaac tcggggcagg ggtggtggag 540

tgcactgagg caggtgttga ggaactctgc agacccctct tccttcccaa agcagccctc 600

tctgctctcc atcgcag 617

<210> 48
<211> 130
<212> DNA
<213> HUMAN

<220>
<221> intron
<222> (1)..(130)
<223> 10th MN intron

<400> 48
gtattacact gacccttttct tcaggcacaa gcttccccca cccttgtgga gtcacttcat 60

gcaaagcgca tgcaaatgag ctgctcctgg gccagttttc tgattagcct ttcctgttgt 120

gtacacacag 130

<210> 49

<211> 1401
<212> DNA
<213> HUMAN

<400> 49
caaactttca cttttgttgc ccaggctgga gtgcaatggc gcgatctcgg ctcactgcaa 60

cctccacctc ccgggttcaa gtgattctcc tgcctcagcc tctagccaag tagctgcgat 120

tacaggcatg cgccaccacg cccggctaat ttttgtattt ttagtagaga cggggtttcg 180

ccatgttggt caggctggtc tcgaactcct gatctcaggt gatccaacca ccctggcctc 240

ccaaagtgct gggattatag gcgtgagcca cagcgcctgg cctgaagcag ccactcactt 300

ttacagaccc taagacaatg attgcaagct ggtaggattg ctgtttggcc cacccagctg 360

cggtgttgag tttgggtgcg gtctcctgtg ctttgcacct ggcccgctta aggcatttgt 420

tacccgtaat gctcctgtaa ggcatctgcg tttgtgacat cgttttggtc gccaggaagg 480

gattggggct ctaagcttga gcggttcatc cttttcattt atacagggga tgaccagagt 540

cattggcgct atggaggtga gacacccacc cgctgcacag acccaatctg ggaacccagc 600

tctgtggatc tcccctacag ccgtccctga acactggtcc cgggcgtccc acccgccgcc 660

caccgtccca ccccctcacc ttttctaccc gggttcccta agttcctgac ctaggcgtca 720

gacttcctca ctatactctc ccaccccagg cgacccgccc tggccccggg tgtccccagc 780

ctgcgcgggc cgcttccagt ccccggtgga tatccgcccc cagctcgccg ccttctgccc 840

ggccctgcgc cccctggaac tcctgggctt ccagctcccg ccgctcccag aactgcgcct 900

gcgcaacaat ggccacagtg gtgagggggt ctccccgccg agacttgggg atggggcggg 960

gcgcagggaa gggaaccgtc gcgcagtgcc tgccccgggg ttgggctggc cctaccgggc 1020

ggggccggct cacttgcctc tccctacgca gtgcaactga ccctgcctcc tgggctagag 1080

atggctctgg gtcccgggcg ggagtaccgg gctctgcagc tgcatctgca ctgggggggct 1140

gcaggtcgtc cgggctcgga gcacactgtg gaaggccacc gtttccctgc cgaggtgagc 1200

gcggactggc cgagaagggg caaaggagcg gggcggacgg gggccagaga cgtggccctc 1260

tcctaccctc gtgtcctttt cagatccacg tggttcacct cagcaccgcc tttgccagag 1320

ttgacgaggc cttggggcgc ccgggaggcc tggccgtgtt ggccgccttt ctggaggtac 1380

cagatcctgg acacccccta c 1401

<210> 50
<211> 59
<212> PRT
<213> HUMAN

<400> 50
Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro Ser Glu
1 5 10 15

Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro
20 25 30

Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu Val Lys Pro
35 40 45

Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu
50 55

<210> 51
<211> 257
<212> PRT
<213> HUMAN

<400> 51
Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp Pro
1 5 10 15

Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp Ile
20 25 30

Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu Leu
35 40 45

Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn Asn
50 55 60

Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala Leu
65 70 75 80

Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp Gly
85 90 95

```
Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg Phe
            100                 105                 110

Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg Val
        115                 120                 125

Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala Phe
    130                 135                 140

Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu Leu Ser
145                 150                 155                 160

Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu Thr Gln Val Pro Gly
                165                 170                 175

Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe Ser Arg Tyr Phe Gln
            180                 185                 190

Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala Gln Gly Val Ile Trp
        195                 200                 205

Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala Lys Gln Leu His Thr
    210                 215                 220

Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu Asn
225                 230                 235                 240

Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser Phe
                245                 250                 255

Pro
```



```
<210> 52
<211> 20
<212> PRT
<213> HUMAN

<400> 52
Ile Leu Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala
  1               5                  10                  15

Phe Leu Val Gln
            20
```

<210> 53
<211> 25
<212> PRT
<213> HUMAN

<400> 53
Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg
1 5 10 15

Pro Ala Glu Val Ala Glu Thr Gly Ala
20 25

<210> 54
<211> 59
<212> PRT
<213> HUMAN

<400> 54
Ser Ala Ser Glu Glu Pro Ser Pro Ser Glu Val Pro Phe Pro Ser Glu
1 5 10 15

Glu Pro Ser Pro Ser Glu Glu Pro Phe Pro Ser Val Arg Pro Phe Pro
20 25 30

Ser Val Val Leu Phe Pro Ser Glu Glu Pro Phe Pro Ser Lys Glu Pro
35 40 45

Ser Pro Ser Glu Glu Pro Ser Ala Ser Glu Glu
50 55

<210> 55
<211> 470
<212> RNA
<213> HUMAN

<400> 55
cauggccccg auaaccuucu gccugugcac acaccugccc cucacuccac ccccauccua 60

gcuuugguau gggggagagg gcacagggcc agacaaaccu gugagacuuu ggcuccaucu 120

cugcaaaagg gcgcucugug agucagccug cuccccucca ggcuugcucc ucccccaccc 180

agcucucguu uccaaugcac guacagcccg uacacaccgu gugcugggac accccacagu 240

cagccgcaug gcucccccugu gccccagccc cuggcucccu cuguugaucc cggccccugc 300

uccaggccuc acugugcaac ugcugcuguc acugcugcuu cuggugccug uccaucccca 360

gagguugccc cggaugcagg aggauucccc cuugggagga ggcucuucug gggaagauga 420

cccacugggc gaggaggauc ugcccaguga agaggauuca cccagagagg 470

<210> 56
<211> 292
<212> DNA
<213> HUMAN

<400> 56
gttttttttga gacggagtct tgcatctgtc atgcccaggc tggagtagca gtggtgccat 60

ctcggctcac tgcaagctcc acctcccgag ttcacgccat tttcctgcct cagcctcccg 120

agtagctggg actacaggcg cccgccacca tgcccggcta atttttttgta tttttggtag 180

agacggggtt tcaccgtgtt agccagaatg gtctcgatct cctgacttcg tgatccaccc 240

gcctcggcct cccaaagttc tgggattaca ggtgtgagcc accgcacctg gc 292

<210> 57
<211> 262
<212> DNA
<213> HUMAN

<400> 57
tttctttttt gagacagggt cttgctctgt cacccaggcc agagtgcaat ggtacagtct 60

cagctcactg cagcctcaac cgcctcggct caaaccatca tcccatttca gcctcctgag 120

tagctgggac tacaggcaca tgccattaca cctggctaat ttttttgtat ttctagtaga 180

gacagggttt ggccatgttg cccgggctgg tctcgaactc ctggactcaa gcaatccacc 240

cacctcagcc tcccaaaatg ag 262

<210> 58
<211> 2501
<212> DNA
<213> HUMAN

<220>
<221> misc_feature

<222> (1)..(2501)

<400> 58

tgttgactcg tgaccttacc cccaaccctg tgctctctga aacatgagct gtgtccactc 60

agggttaaat ggattaaggg cggtgcaaga tgtgctttgt taaacagatg cttgaaggca 120

gcatgctcgt taagagtcat caccaatccc taatctcaag taatcaggga cacaaacact 180

gcggaaggcc gcagggtcct ctgcctagga aaaccagaga cctttgttca cttgtttatc 240

tgaccttccc tccactattg tccatgaccc tgccaaatcc ccctctgtga gaaacaccca 300

agaattatca ataaaaaaat aaatttaaaa aaaaaataca aaaaaaaaaa aaaaaaaaaa 360

aaaagactta cgaatagtta ttgataaatg aatagctatt ggtaaagcca agtaaatgat 420

catattcaaa accagacggc catcatcaca gctcaagtct acctgatttg atctctttat 480

cattgtcatt ctttggattc actagattag tcatcatcct caaaattctc ccccaagttc 540

taattacgtt ccaaacattt aggggttaca tgaagcttga acctactacc ttctttgctt 600

ttgagccatg agttgtagga atgatgagtt tacaccttac atgctgggga ttaatttaaa 660

ctttacctct aagtcagttg ggtagccttt ggcttatttt tgtagctaat tttgtagtta 720

atggatgcac tgtgaatctt gctatgatag ttttcctcca cactttgcca ctaggggtag 780

gtaggtactc agttttcagt aattgcttac ctaagaccct aagccctatt tctcttgtac 840

tggcctttat ctgtaatatg ggcatattta atacaatata atttttggag ttttttttgtt 900

tgtttgtttg tttgtttttt tgagacggag tcttgcatct gtcatgccca ggctggagta 960

gcagtggtgc catctcggct cactgcaagc tccacctccc gagttcacgc cattttcctg 1020

cctcagcctc ccgagtagct gggactacag gcgcccgcca ccatgcccgg ctaatttttt 1080

gtatttttgg tagagacggg gtttcaccgt gttagccaga atggtctcga tctcctgact 1140

tcgtgatcca cccgcctcgg cctcccaaag ttctgggatt acaggtgtga gccaccgcac 1200

ctggccaatt ttttgagtct tttaaagtaa aaatatgtct tgtaagctgg taactatggt 1260

acatttcctt ttattaatgt ggtgctgacg gtcatatagg ttcttttgag tttggcatgc 1320

atatgctact ttttgcagtc ctttcattac atttttctct cttcatttga agagcatgtt 1380

atatctttta gcttcacttg gcttaaaagg ttctctcatt agcctaacac agtgtcattg 1440

ttggtaccac ttggatcata agtggaaaaa cagtcaagaa attgcacagt aatacttgtt 1500

tgtaagaggg atgattcagg tgaatctgac actaagaaac tcccctacct gaggtctgag 1560

attcctctga cattgctgta tataggcttt tcctttgaca gcctgtgact gcggactatt 1620

tttcttaagc aagatatgct aaagttttgt gagccttttt ccagagagag gtctcatatc 1680

tgcatcaagt gagaacatat aatgtctgca tgtttccata tttcaggaat gtttgcttgt 1740

gttttatgct tttatataga cagggaaact tgttcctcag tgacccaaaa gaggtgggaa 1800

ttgttattgg atatcatcat tggcccacgc tttctgacct tggaaacaat taagggttca 1860

taatctcaat tctgtcagaa ttggtacaag aaatagctgc tatgtttctt gacattccac 1920

ttggtaggaa ataagaatgt gaaactcttc agttggtgtg tgtccctngt ttttttgcaa 1980

tttccttctt actgtgttaa aaaaaagtat gatcttgctc tgagaggtga ggcattctta 2040

atcatgatct ttaaagatca ataatataat cctttcaagg attatgtctt tattataata 2100

aagataattt gtctttaaca gaatcaataa tataatccct taaaggatta tatctttgct 2160

gggcgcagtg gctcacacct gtaatcccag cactttgggt ggccaaggtg gaaggatcaa 2220

atttgcctac ttctatatta tcttctaaag cagaattcat ctctcttccc tcaatatgat 2280

gatattgaca gggtttgccc tcactcacta gattgtgagc tcctgctcag ggcaggtagc 2340

gtttttttgtt tttgtttttg tttttctttt ttgagacagg gtcttgctct gtcacccagg 2400

ccagagtgca atggtacagt ctcagctcac tgcagcctca accgcctcgg ctcaaaccat 2460

catcccattt cagcctcctg agtagctggg actacaggca c 2501

<210> 59
<211> 292
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)

<400> 59
ttttttgag acggagtctt gcatctgtca tgcccaggct ggagtagcag tggtgccatc 60

tcggctcact gcaagctcca cctcccgagt tcacgccatt ttcctgcctc agcctcccga 120

gtagctggga ctacaggcgc ccgccaccat gcccggctaa ttttttgtat ttttggtaga 180

gacggggttt caccgtgtta gccagaatgg tctcgatctc ctgacttcgt gatccacccg 240

cctcggcctc ccaaagttct gggattacag gtgtgagcca ccgcacctgg cc 292

<210> 60
<211> 262
<212> DNA
<213> HUMAN

<400> 60
ttctttttttg agacagggtc ttgctctgtc acccaggcca gagtgcaatg gtacagtctc 60

agctcactgc agcctcaacc gcctcggctc aaaccatcat cccatttcag cctcctgagt 120

agctgggact acaggcacat gccattacac ctggctaatt tttttgtatt tctagtagag 180

acagggtttg gccatgttgc ccgggctggt ctcgaactcc tggactcaag caatccaccc 240

acctcagcct cccaaaatga gg 262

<210> 61
<211> 294
<212> DNA
<213> HUMAN

<400> 61
tttttttttg agacaaactt tcacttttgt tgcccaggct ggagtgcaat ggcgcgatct 60

cggctcactg caacctccac ctcccgggtt caagtgattc tcctgcctca gcctctagcc 120

aagtagctgc gattacaggc atgcgccacc acgcccggct aatttttgta tttttagtag 180

agacggggtt tcgccatgtt ggtcaggctg gtctcgaact cctgatctca ggtgatccaa 240

ccaccctggc ctcccaaagt gctgggatta taggcgtgag ccacagcgcc tggc 294

<210> 62

<211> 276
<212> DNA
<213> HUMAN

<400> 62
tgacagtctc tctgtcgccc aggctggagt gcagtggtgt gatcttgggt cactgcaact 60

tccgcctccc gggttcaagg gattctcctg cctcagcttc ctgagtagct ggggttacag 120

gtgtgtgcca ccatgcccag ctaatttttt tttgtatttt tagtagacag ggtttcacca 180

tgttggtcag gctggtctca aactcctggc ctcaagtgat ccgcctgact cagcctacca 240

aagtgctgat tacaagtgtg agccaccgtg cccagc 276

<210> 63
<211> 289
<212> DNA
<213> HUMAN

<400> 63
cgccgggcac ggtggctcac gcctgtaatc ccagcacttt gggaggccaa ggcaggtgga 60

tcacgaggtc aagagatcaa gaccatcctg gccaacatgg tgaaacccca tctctactaa 120

aaatacgaaa aaatagccag gcgtggtggc gggtgcctgt aatcccagct actcgggagg 180

ctgaggcagg agaatggcat gaacccggga ggcagaagtt gcagtgagcc gagatcgtgc 240

cactgcactc cagcctgggc aacagagcga gactcttgtc tcaaaaaaa 289

<210> 64
<211> 298
<212> DNA
<213> HUMAN

<400> 64
aggctgggct ctgtggctta cgcctataat cccaccacgt tgggaggctg aggtgggaga 60

atggtttgag cccaggagtt caagacaagg cggggcaaca tagtgtgacc ccatctctac 120

caaaaaaacc ccaacaaaac caaaaatagc cgggcatggt ggtatgcggc ctagtcccag 180

ctactcaagg aggctgaggt gggaagatcg cttgattcca ggagtttgag actgcagtga 240

gctatgatcc caccactgcc taccatcttt aggatacatt tatttattta taaaagaa 298

<210> 65
<211> 105
<212> DNA
<213> HUMAN

<400> 65
tttttttacat ctttagtaga gacagggttt caccatattg gccaggctgc tctcaaactc 60

ctgaccttgt gatccaccag cctcggcctc ccaaagtgct gggat 105

<210> 66
<211> 83
<212> DNA
<213> HUMAN

<400> 66
cctcgaactc ctaggctcag gcaatccttt caccttagct tctcaaagca ctgggactgt 60

aggcatgagc cactgtgcct ggc 83

<210> 67
<211> 11
<212> DNA
<213> HUMAN

<400> 67
agaaggtaag t 11

<210> 68
<211> 11
<212> DNA
<213> HUMAN

<400> 68
tggaggtgag a 11

<210> 69
<211> 11
<212> DNA
<213> HUMAN

<400> 69

cagtcgtgag g 11

<210> 70
<211> 11
<212> DNA
<213> HUMAN

<400> 70
ccgaggtgag c 11

<210> 71
<211> 11
<212> DNA
<213> HUMAN

<400> 71
tggaggtacc a 11

<210> 72
<211> 11
<212> DNA
<213> HUMAN

<400> 72
ggaaggtcag t 11

<210> 73
<211> 11
<212> DNA
<213> HUMAN

<400> 73
agcaggtggg c 11

<210> 74
<211> 11
<212> DNA
<213> HUMAN

<400> 74
gccaggtaca g 11

<210> 75
<211> 11
<212> DNA
<213> HUMAN

<400> 75
tgctggtgag t 11

<210> 76
<211> 11
<212> DNA
<213> HUMAN

<400> 76
atacagggga t 11

<210> 77
<211> 11
<212> DNA
<213> HUMAN

<400> 77
atacagggga t 11

<210> 78
<211> 11
<212> DNA
<213> HUMAN

<400> 78
ccccaggcga c 11

<210> 79
<211> 11
<212> DNA
<213> HUMAN

<400> 79
acgcagtgca a 11

<210> 80
<211> 11
<212> DNA

<213> HUMAN

<400> 80
tttcagatcc a 11

<210> 81
<211> 11
<212> DNA
<213> HUMAN

<400> 81
ccccaggagg g 11

<210> 82
<211> 11
<212> DNA
<213> HUMAN

<400> 82
tcacaggctc a 11

<210> 83
<211> 11
<212> DNA
<213> HUMAN

<400> 83
ccctagctcc a 11

<210> 84
<211> 11
<212> DNA
<213> HUMAN

<400> 84
ctccagtcca g 11

<210> 85
<211> 12
<212> DNA
<213> HUMAN

<400> 85

tcgcaggtga ca 12

<210> 86
<211> 11
<212> DNA
<213> HUMAN

<400> 86
acacagaagg g 11

<210> 87
<211> 377
<212> PRT
<213> HUMAN

<400> 87

```
Gln Arg Leu Pro Arg Met Gln Glu Asp Ser Pro Leu Gly Gly Gly Ser
  1               5                  10                  15

Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro Ser Glu Glu
             20                  25                  30

Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro Gly
         35                  40                  45

Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu Val Lys Pro Lys
     50                  55                  60

Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu Asp Leu Pro Thr Val Glu
 65                  70                  75                  80

Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys
                 85                  90                  95

Glu Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp
            100                 105                 110

Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp
        115                 120                 125

Ile Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu
    130                 135                 140

Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn
145                 150                 155                 160
```

```
Asn Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala
                165                 170                 175

Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp
            180                 185                 190

Gly Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg
        195                 200                 205

Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg
    210                 215                 220

Val Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala
225                 230                 235                 240

Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu Leu
                245                 250                 255

Ser Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu Thr Gln Val Pro
            260                 265                 270

Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe Ser Arg Tyr Phe
        275                 280                 285

Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala Gln Gly Val Ile
    290                 295                 300

Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala Lys Gln Leu His
305                 310                 315                 320

Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu
                325                 330                 335

Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser
            340                 345                 350

Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln
        355                 360                 365

Leu Asn Ser Cys Leu Ala Ala Gly Asp
    370                 375
```

<210> 88
<211> 34
<212> DNA
<213> HUMAN

<400> 88
tagacagatc tacgatggct cccctgtgcc ccag 34

<210> 89
<211> 34
<212> DNA
<213> HUMAN

<400> 89
attcctctag acagttaccg gctccccctc agat 34

<210> 90
<211> 3532
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(3532)

<400> 90
tgttgactcg tgaccttacc cccaaccctg tgctctctga aacatgagct gtgtccactc 60

agggttaaat ggattaaggg cggtgcaaga tgtgctttgt taaacagatg cttgaaggca 120

gcatgctcgt taagagtcat caccaatccc taatctcaag taatcaggga cacaaacact 180

gcggaaggcc gcagggtcct ctgcctagga aaaccagaga cctttgttca cttgtttatc 240

tgaccttccc tccactattg tccatgaccc tgccaaatcc ccctctgtga gaaacaccca 300

agaattatca ataaaaaaat aaatttaaaa aaaaaatnca aaaaaaaaaa aaaaaaaaaa 360

aaaagactta cgaatagtta ttgataaatg aatagctatt ggtaaagcca agtaaatgat 420

catattcaaa accagacggc catcatcaca gctcaagtct acctgatttg atctctttat 480

cattgtcatt ctttggattc actagattag tcatcatcct caaaattctc ccccaagttc 540

taattacgtt ccaaacattt aggggttaca tgaagcttga acctactacc ttctttgctt 600

ttgagccatg agttgtagga atgatgagtt tacaccttac atgctgggga ttaatttaaa 660

ctttacctct aagtcagttg ggtagccttt ggcttatttt tgtagctaat tttgtagtta 720

atggatgcac tgtgaatctt gctatgatag ttttcctcca cactttgcca ctaggggtag 780

gtaggtactc agttttcagt aattgcttac ctaagaccct aagccctatt tctcttgtac 840

tggcctttat ctgtaatatg ggcatattta atacaatata atttttggag ttttttttgtt 900

tgtttgtttg tttgtttttt tgagacggag tcttgcatct gtcatgccca ggctggagta 960

gcagtggtgc catctcggct cactgcaagc tccacctccc gagttcacgc cattttcctg 1020

cctcagcctc ccgagtagct gggactacag gcgcccgcca ccatgcccgg ctaatttttt 1080

gtatttttgg tagagacggg gtttcaccgt gttagccaga atggtctcga tctcctgact 1140

tcgtgatcca cccgcctcgg cctcccaaag ttctgggatt acaggtgtga gccaccgcac 1200

ctggccaatt ttttgagtct tttaaagtaa aaatatgtct tgtaagctgg taactatggt 1260

acatttcctt ttattaatgt ggtgctgacg gtcatatagg ttcttttgag tttggcatgc 1320

atatgctact ttttgcagtc ctttcattac atttttctct cttcatttga agagcatgtt 1380

atatctttta gcttcacttg gcttaaaagg ttctctcatt agcctaacac agtgtcattg 1440

ttggtaccac ttggatcata agtggaaaaa cagtcaagaa attgcacagt aatacttgtt 1500

tgtaagaggg atgattcagg tgaatctgac actaagaaac tcccctacct gaggtctgag 1560

attcctctga cattgctgta tataggcttt tcctttgaca gcctgtgact gcggactatt 1620

tttcttaagc aagatatgct aaagttttgt gagccttttt ccagagagag gtctcatatc 1680

tgcatcaagt gagaacatat aatgtctgca tgtttccata tttcaggaat gtttgcttgt 1740

gttttatgct tttatataga cagggaaact tgttcctcag tgacccaaaa gaggtgggaa 1800

ttgttattgg atatcatcat tggcccacgc tttctgacct tggaaacaat taagggttca 1860

taatctcaat tctgtcagaa ttggtacaag aaatagctgc tatgtttctt gacattccac 1920

ttggtaggaa ataagaatgt gaaactcttc agttggtgtg tgtccctngt ttttttgcaa 1980

tttccttctt actgtgttaa aaaaaagtat gatcttgctc tgagaggtga ggcattctta 2040

atcatgatct ttaaagatca ataatataat cctttcaagg attatgtctt tattataata 2100

aagataattt gtctttaaca gaatcaataa tataatccct taaaggatta tatctttgct 2160

gggcgcagtg gctcacacct gtaatcccag cactttgggt ggccaaggtg gaaggatcaa 2220

atttgcctac ttctatatta tcttctaaag cagaattcat ctctcttccc tcaatatgat 2280

gatattgaca gggtttgccc tcactcacta gattgtgagc tcctgctcag ggcaggtagc 2340

gttttttgtt tttgtttttg ttttttcttt ttgagacagg gtcttgctct gtcacccagg 2400

ccagagtgca atggtacagt ctcagctcac tgcagcctca accgcctcgg ctcaaaccat 2460

catcccattt cagcctcctg agtagctggg actacaggca catgccatta cacctggcta 2520

atttttttgt atttctagta gagacagggt ttggccatgt tgcccgggct ggtctcgaac 2580

tcctggactc aagcaatcca cccacctcag cctcccaaaa tgagggaccg tgtcttattc 2640

atttccatgt ccctagtcca tagcccagtg ctggacctat ggtagtacta aataaatatt 2700

tgttgaatgc aatagtaaat agcatttcag ggagcaagaa ctagattaac aaaggtggta 2760

aaaggtttgg agaaaaaaat aatagtttaa tttggctaga gtatgaggga gagtagtagg 2820

agacaagatg gaaaggtctc ttgggcaagg ttttgaagga agttggaagt cagaagtaca 2880

caatgtgcat atcgtggcag gcagtgggga gccaatgaag gcttttgagc aggagagtaa 2940

tgtgttgaaa aataaatata ggttaaacct atcagagccc ctctgacaca tacacttgct 3000

tttcattcaa gctcaagttt gtctcccaca tacccattac ttaactcacc ctcgggctcc 3060

cctagcagcc tgccctacct ctttacctgc ttcctggtgg agtcagggat gtatacatga 3120

gctgctttcc ctctcagcca gaggacatgg ggggccccag ctcccctgcc tttccccttc 3180

tgtgcctgga gctgggaagc aggccagggt tagctgaggc tggctggcaa gcagctgggt 3240

ggtgccaggg agagcctgca tagtgccagg tggtgccttg ggttccaagc tagtccatgg 3300

ccccgataac cttctgcctg tgcacacacc tgcccctcac tccaccccca tcctagcttt 3360

ggtatggggg agagggcaca gggccagaca aacctgtgag actttggctc catctctgca 3420

aaagggcgct ctgtgagtca gcctgctccc ctccaggctt gctcctcccc cacccagctc 3480

tcgtttccaa tgcacgtaca gcccgtacac accgtgtgct gggacacccc ac 3532

<210> 91
<211> 204

<212> DNA
<213> HUMAN

<400> 91
cctgcccctc actccacccc catcctagct ttggtatggg ggagagggca cagggccaga 60

caaacctgtg agactttggc tccatctctg caaaagggcg ctctgtgagt cagcctgctc 120

ccctccaggc ttgctcctcc cccacccagc tctcgtttcc aatgcacgta cagcccgtac 180

acaccgtgtg ctgggacacc ccac 204

<210> 92
<211> 132
<212> DNA
<213> HUMAN

<400> 92
ggatcctgtt gactcgtgac cttaccccca accctgtgct ctctgaaaca tgagctgtgt 60

ccactcaggg ttaaatggat taagggcggt gcaagatgtg ctttgttaaa cagatgcttg 120

aaggcagcat gc 132

<210> 93
<211> 275
<212> DNA
<213> HUMAN

<400> 93
gcatagtgcc aggtggtgcc ttgggttcca agctagtcca tggccccgat aaccttctgc 60

ctgtgcacac acctgcccct cactccaccc ccatcctagc tttggtatgg gggagagggc 120

acagggccag acaaacctgt gagactttgg ctccatctct gcaaaagggc gctctgtgag 180

tcagcctgct cccctccagg cttgctcctc ccccacccag ctctcgtttc caatgcacgt 240

acagcccgta cacaccgtgt gctgggacac cccac 275

<210> 94
<211> 89
<212> DNA
<213> HUMAN

<400> 94
ctgctcccct ccaggcttgc tcctccccca cccagctctc gtttccaatg cacgtacagc 60

ccgtacacac cgtgtgctgg gacacccca 89

<210> 95
<211> 61
<212> DNA
<213> HUMAN

<400> 95
cacccagctc tcgtttccaa tgcacgtaca gcccgtacac accgtgtgct gggacacccc 60

a 61

<210> 96
<211> 116
<212> DNA
<213> HUMAN

<400> 96
acctgccccc cactccaccc ccatcctagc tttggtatgg gggagagggc acagggccag 60

acaaacctgt gagactttgg ctccatctct gcaaaagggc gctctgtgag tcagcc 116

<210> 97
<211> 36
<212> PRT
<213> HUMAN

<400> 97
Gly Glu Glu Asp Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp
1 5 10 15

Pro Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu
20 25 30

Glu Asp Leu Pro
35

<210> 98
<211> 6
<212> PRT
<213> HUMAN

<400> 98
Gly Glu Glu Asp Leu Pro
1 5

<210> 99
<211> 4
<212> PRT
<213> HUMAN

<400> 99
Glu Glu Asp Leu
1

<210> 100
<211> 5
<212> PRT
<213> HUMAN

<400> 100
Glu Glu Asp Leu Pro
1 5

<210> 101
<211> 6
<212> PRT
<213> HUMAN

<400> 101
Glu Asp Leu Pro Ser Glu
1 5

<210> 102
<211> 7
<212> PRT
<213> HUMAN

<400> 102
Glu Glu Asp Leu Pro Ser Glu
1 5

<210> 103
<211> 6

<212> PRT
<213> HUMAN

<400> 103
Asp Leu Pro Gly Glu Glu
1 5

<210> 104
<211> 22
<212> PRT
<213> HUMAN

<400> 104
Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro
1 5 10 15

Ser Glu Glu Asp Ser Pro
20

<210> 105
<211> 25
<212> PRT
<213> HUMAN

<400> 105
Gly Glu Glu Asp Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp
1 5 10 15

Pro Pro Gly Glu Glu Asp Leu Pro Gly
20 25

<210> 106
<211> 24
<212> PRT
<213> HUMAN

<400> 106
Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
1 5 10 15

Gly Glu Glu Asp Leu Pro Glu Val
20

<210> 107

<211> 7
<212> PRT
<213> HUMAN

<400> 107
Gly Glu Thr Arg Ala Pro Leu
1 5

<210> 108
<211> 7
<212> PRT
<213> HUMAN

<400> 108
Gly Glu Thr Arg Glu Pro Leu
1 5

<210> 109
<211> 7
<212> PRT
<213> HUMAN

<400> 109
Gly Gln Thr Arg Ser Pro Leu
1 5

<210> 110
<211> 1247
<212> DNA
<213> HUMAN

<220>
<221> misc_feature
<222> (1)..(1247)

<400> 110
tatgctactt tttgcagtcc tttcattaca ttttttctctc ttcatttgaa gagcatgtta 60

tatcttttag cttcacttgg cttaaaaggt tctctcatta gcctaacaca gtgtcattgt 120

tggtaccact tggatcataa gtggaaaaac agtcaagaaa ttgcacagta atacttgttt 180

gtaagaggga tgattcaggt gaatctgaca ctaagaaact cccctacctg aggtctgaga 240

ttcctctgac attgctgtat ataggctttt cctttgacag cctgtgactg cggactattt 300

ttcttaagca agatatgcta aagttttgtg agccttttc cagagagagg tctcatatct 360

gcatcaagtg agaacatata atgtctgcat gtttccatat ttcaggaatg tttgcttgtg 420

ttttatgctt ttatatagac agggaaactt gttcctcagt gacccaaaag aggtgggaat 480

tgttattgga tatcatcatt ggcccacgct ttctgacctt ggaaacaatt aagggttcat 540

aatctcaatt ctgtcagaat tggtacaaga aatagctgct atgtttcttg acattccact 600

tggtaggaaa taagaatgtg aaactcttca gttggtgtgt gtccctngtt tttttgcaat 660

ttccttctta ctgtgttaaa aaaaagtatg atcttgctct gagaggtgag gcattcttaa 720

tcatgatctt taaagatcaa taatataatc ctttcaagga ttatgtcttt attataataa 780

agataatttg tctttaacag aatcaataat ataatccctt aaaggattat atctttgctg 840

ggcgcagtgg ctcacacctg taatcccagc actttgggtg gccaaggtgg aaggatcaaa 900

tttgcctact tctatattat cttctaaagc agaattcatc tctcttccct caatatgatg 960

atattgacag ggtttgccct cactcactag attgtgagct cctgctcagg gcaggtagcg 1020

ttttttgttt ttgtttttgt ttttcttttt tgagacaggg tcttgctctg tcacccaggc 1080

cagagtgcaa tggtacagtc tcagctcact gcagcctcaa ccgcctcggc tcaaaccatc 1140

atcccatttc agcctcctga gtagctggga ctacaggcac atgccattac acctggctaa 1200

tttttttgta tttctagtag agacagggtt tggccatgtt gcccggg 1247

<210> 111
<211> 17
<212> DNA
<213> HUMAN

<400> 111
ctctgtgagt cagcctg 17

<210> 112
<211> 23
<212> DNA
<213> HUMAN

<400> 112
aggcttgctc ctcccccacc cag 23

<210> 113
<211> 18
<212> DNA
<213> HUMAN

<400> 113
agactttggc tccatctc 18

<210> 114
<211> 20
<212> DNA
<213> HUMAN

<400> 114
cactccaccc ccatcctagc 20

<210> 115
<211> 26
<212> DNA
<213> HUMAN

<400> 115
gggagagggc acagggccag acaaac 26

<210> 116
<211> 20
<212> PRT
<213> HUMAN

<400> 116
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly
1 5 10 15

Gly Gly Gly Ser
20

<210> 117
<211> 34
<212> DNA
<213> HUMAN

<400> 117
cgtctagaag gaattcagct agactggctc agca 34

<210> 118
<211> 15
<212> PRT
<213> HUMAN

<400> 118
Glu Val Lys Pro Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu
1 5 10 15

<210> 119
<211> 12
<212> PRT
<213> HUMAN

<400> 119
Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
1 5 10

<210> 120
<211> 12
<212> PRT
<213> HUMAN

<400> 120
Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly
1 5 10

<210> 121
<211> 10
<212> PRT
<213> HUMAN

<400> 121
Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro
1 5 10

<210> 122
<211> 12
<212> PRT

<213> HUMAN

<400> 122
Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu
1 5 10

<210> 123
<211> 12
<212> PRT
<213> HUMAN

<400> 123
Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp
1 5 10

<210> 124
<211> 12
<212> PRT
<213> HUMAN

<400> 124
Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu
1 5 10

<210> 125
<211> 9
<212> PRT
<213> HUMAN

<400> 125
Ala Pro Gly Glu Glu Asp Leu Pro Ala
1 5

<210> 126
<211> 9
<212> PRT
<213> HUMAN

<400> 126
Ala Gly Glu Glu Asp Leu Pro Gly Ala
1 5

<210> 127

<211> 9
<212> PRT
<213> HUMAN

<400> 127
Ala Glu Glu Asp Leu Pro Gly Glu Ala
1 5

<210> 128
<211> 9
<212> PRT
<213> HUMAN

<400> 128
Ala Glu Asp Leu Pro Gly Glu Glu Ala
1 5

<210> 129
<211> 9
<212> PRT
<213> HUMAN

<400> 129
Ala Asp Leu Pro Gly Glu Glu Asp Ala
1 5

<210> 130
<211> 9
<212> PRT
<213> HUMAN

<400> 130
Ala Leu Pro Gly Glu Glu Asp Leu Ala
1 5

<210> 131
<211> 8
<212> PRT
<213> HUMAN

<400> 131
Ala Gly Glu Glu Asp Leu Pro Ala
1 5

<210> 132
<211> 8
<212> PRT
<213> HUMAN

<400> 132
Ala Glu Glu Asp Leu Pro Gly Ala
1 5

<210> 133
<211> 8
<212> PRT
<213> HUMAN

<400> 133
Ala Glu Asp Leu Pro Gly Glu Ala
1 5

<210> 134
<211> 8
<212> PRT
<213> HUMAN

<400> 134
Ala Asp Leu Pro Gly Glu Glu Ala
1 5

<210> 135
<211> 8
<212> PRT
<213> HUMAN

<400> 135
Ala Leu Pro Gly Glu Glu Asp Ala
1 5

<210> 136
<211> 8
<212> PRT
<213> HUMAN

<400> 136
Ala Pro Gly Glu Glu Asp Leu Ala

1 5

<210> 137
<211> 9
<212> PRT
<213> HUMAN

<400> 137
Ala Lys Lys Met Lys Arg Arg Lys Ala
1 5

<210> 138
<211> 9
<212> PRT
<213> HUMAN

<400> 138
Ala Ile Thr Phe Asn Ala Gln Tyr Ala
1 5

<210> 139
<211> 9
<212> PRT
<213> HUMAN

<400> 139
Ala Ser Ala Ser Ala Pro Val Ser Ala
1 5

<210> 140
<211> 9
<212> PRT
<213> HUMAN

<400> 140
Ala Gly Gln Thr Arg Ser Pro Leu Ala
1 5

<210> 141
<211> 6
<212> PRT
<213> HUMAN

<400> 141
Ser Glu Glu Asp Ser Pro
1 5

<210> 142
<211> 6
<212> PRT
<213> HUMAN

<400> 142
Arg Glu Glu Asp Pro Pro
1 5

<210> 143
<211> 12
<212> DNA
<213> HUMAN

<400> 143
agggcacagg gc 12